

FIG. 1A

FIG. 1B

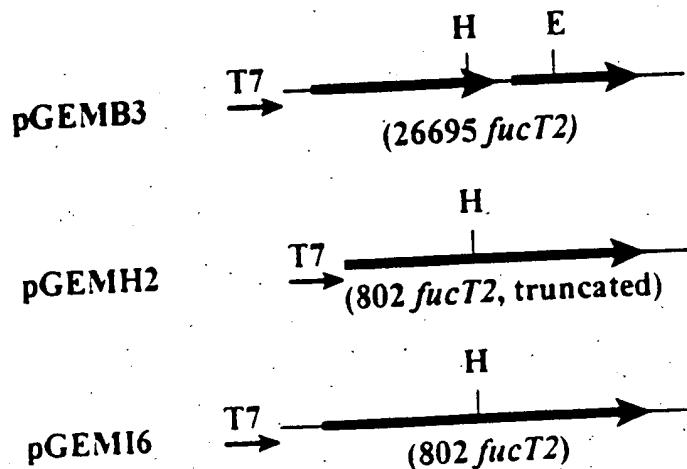
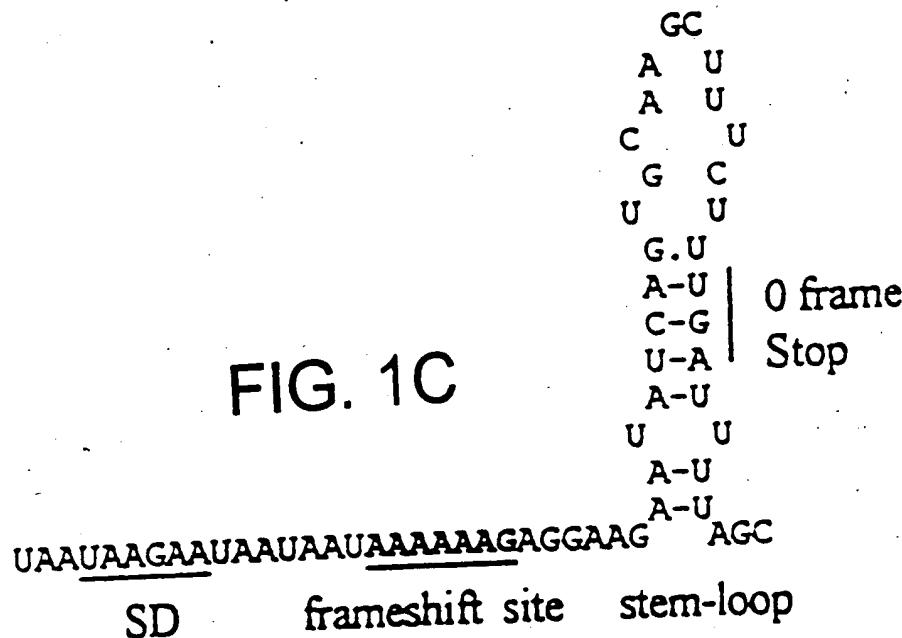


FIG. 3A

gaacactcac acgcgtctt ttcaaataaa aaattcaaat gatggaaag cgtaaaaa 60  
 ctttttaggc ttttattgaa aaaggcgtt aaagttggct aaaataggcg ttttatttga 120  
 aaaacaaagg ggttga atg gct ttt aaa gtt gtt caa att tgt ggg ggg ctt 172  
 Met Ala Phe Lys Val Val Gln Ile Cys Gly Gly Leu  
 1 5 10  
 ggg aat caa atg ttt caa tac gct ttc gct aaa agt ttg caa aaa cac 220  
 Gly Asn Gln Met Phe Gln Tyr Ala Phe Ala Lys Ser Leu Gln Lys His  
 15 20 25  
 ctt aat acg ccc gtc cta tta gac act act tct ttt gat tgg agc aat 268  
 Leu Asn Thr Pro Val Leu Leu Asp Thr Thr Ser Phe Asp Trp Ser Asn  
 30 35 40  
 agg aaa atg caa tta gag ctt ttc cct att gat ttg ccc tat gcg aat 316  
 Arg Lys Met Gln Leu Glu Leu Phe Pro Ile Asp Leu Pro Tyr Ala Asn  
 45 50 55 60  
 gca aaa gaa atc gct ata gct aaa atg caa cat ctc ccc aag tta gta 364  
 Ala Lys Glu Ile Ala Ile Ala Lys Met Gln His Leu Pro Lys Leu Val  
 65 70 75  
 aga gat gca ctc aaa tac ata gga ttt gat agg gtc agt caa gaa atc 412  
 Arg Asp Ala Leu Lys Tyr Ile Gly Phe Asp Arg Val Ser Gln Glu Ile  
 80 85 90  
 gtt ttt gaa tac gag cct aaa ttg tta aag cca agc cgt ttg act tat 460  
 Val Phe Glu Tyr Glu Pro Lys Leu Leu Lys Pro Ser Arg Leu Thr Tyr  
 95 100 105  
 ttt ttt ggc tat ttc caa gat cca cga tat ttt gat gct ata tcc tct 508  
 Phe Phe Gly Tyr Phe Gln Asp Pro Arg Tyr Phe Asp Ala Ile Ser Ser  
 110 115 120  
 tta atc aag caa acc ttc act cta ccc ccc ccc ccc gaa aat aat aaa 556  
 Leu Ile Lys Gln Thr Phe Thr Leu Pro Pro Pro Glu Asn Asn Lys  
 125 130 135 140  
 aat aat aat aaa aaa gag gaa gaa tac cag cgc aag ctt tct ttg att 604  
 Asn Asn Asn Lys Glu Glu Glu Tyr Gln Arg Lys Leu Ser Leu Ile  
 145 150 155  
 tta gcc gct aaa aac agc gta ttt gtc cat ata aga aga ggg gat tat 652  
 Leu Ala Ala Lys Asn Ser Val Phe Val His Ile Arg Arg Gly Asp Tyr  
 160 165 170  
 gtc ggg att ggc tgt cag ctt ggt att gat tat caa aaa aag gcg ctt 700  
 Val Gly Ile Gly Cys Gln Leu Gly Ile Asp Tyr Gln Lys Lys Ala Leu  
 175 180 185  
 gag tat atg gca aag cgc gtc cca aac atg gag ctt ttt gtc ttt tgc 748  
 Glu Tyr Met Ala Lys Arg Val Pro Asn Met Glu Leu Phe Val Phe Cys  
 190 195 200  
 gaa gac tta aaa ttc acg caa aat ctt gat ctt ggc tac cct ttc acg 796  
 Glu Asp Leu Lys Phe Thr Gln Asn Leu Asp Leu Gly Tyr Pro Phe Thr  
 205 210 215 220  
 gac atg acc act agg gat aaa gaa gaa gag ggc tat tgg gat atg ctg 844  
 Asp Met Thr Thr Arg Asp Lys Glu Glu Ala Tyr Trp Asp Met Leu  
 225 230 235  
 ctc atg caa tct tgc aag cat ggc att atc gct aat agc act tat agc 892  
 Leu Met Gln Ser Cys Lys His Gly Ile Ile Ala Asn Ser Thr Tyr Ser  
 240 245 250  
 tgg tgg gcg gct tat ttg atg gaa aat cca gaa aaa atc att att ggc 940  
 Trp Trp Ala Ala Tyr Leu Met Glu Asn Pro Glu Lys Ile Ile Ile Gly  
 255 260 265  
 ccc aaa cac tgg ctt ttt ggg cat gaa aat att ctt tgt aag gaa tgg 988  
 Pro Lys His Trp Leu Phe Gly His Glu Asn Ile Leu Cys Lys Glu Trp  
 270 275 280  
 gtg aaa ata gaa tcc cat ttt gag gta aaa tcc caa aaa tat aac gct 1036  
 Val Lys Ile Glu Ser His Phe Glu Val Lys Ser Gln Lys Tyr Asn Ala  
 285 290 295 300  
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 ttatagcga gcgctcaatt cta 1119

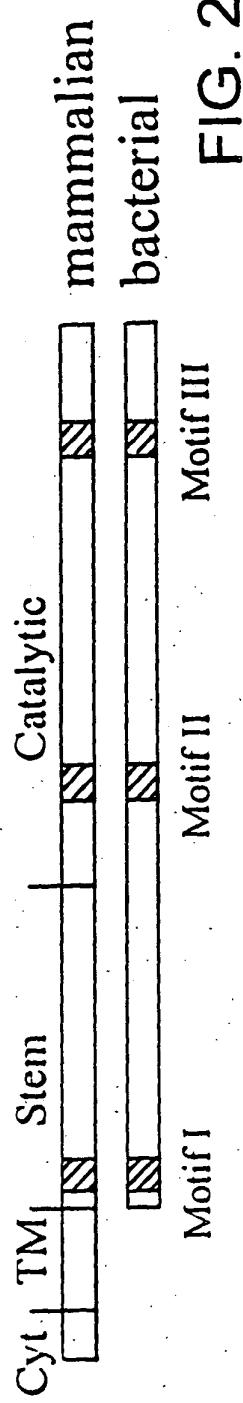


FIG. 2A

	<u>Motif I</u>	<u>Motif II</u>	<u>Motif III</u>
man Fut1 (365 aa)	GRFGNQMGQXA (87-97)	VGVHVRRGDXL (215-225)	GTFGEWAAYL (308-317)
man Fut2 (343 aa)	GRLGNQMGEYA (70-80)	VGVHVRRGDXV (196-206)	GTFGIWAAYL (289-298)
Hp FucT2 (300 aa)	GGLGNQMFAQYA (10-20)	VFVHIRRGDXV (163-173)	STYSWWAAAYL (249-258)
Ye Wbch (283 aa)	GGLGNQLEQVA ( 9-19)	VGIHIRRGDFV (158-168)	STFSSWWAAIL (241-250)
L1 EpsH (309 aa)	GNLGNQLFYIYA ( 8-18)	ICVSIIRRGDXV (173-183)	SSFSWWTEFL (263-272)

FIG. 2B

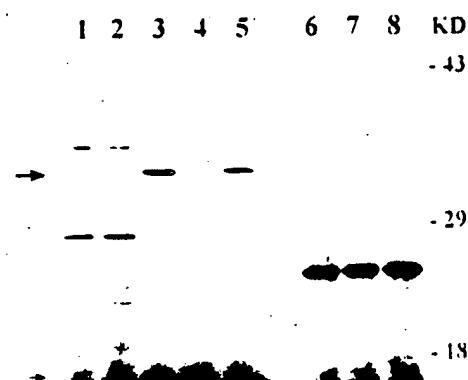


FIG. 3B

UA802 wt

$\Delta H$

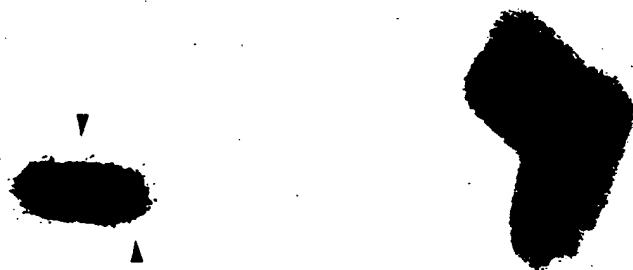


FIG. 4

26695            UA802  
WT  $\Delta H$   $\Delta E$     WT  $\Delta H$   $\Delta E$

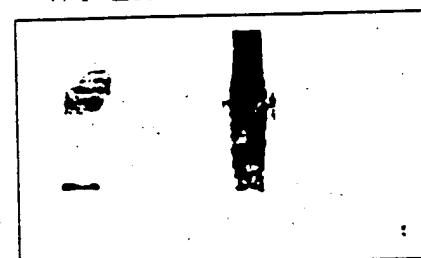


FIG. 6A

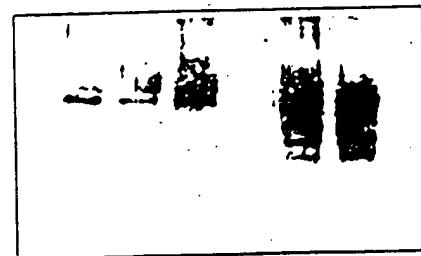


FIG. 6B

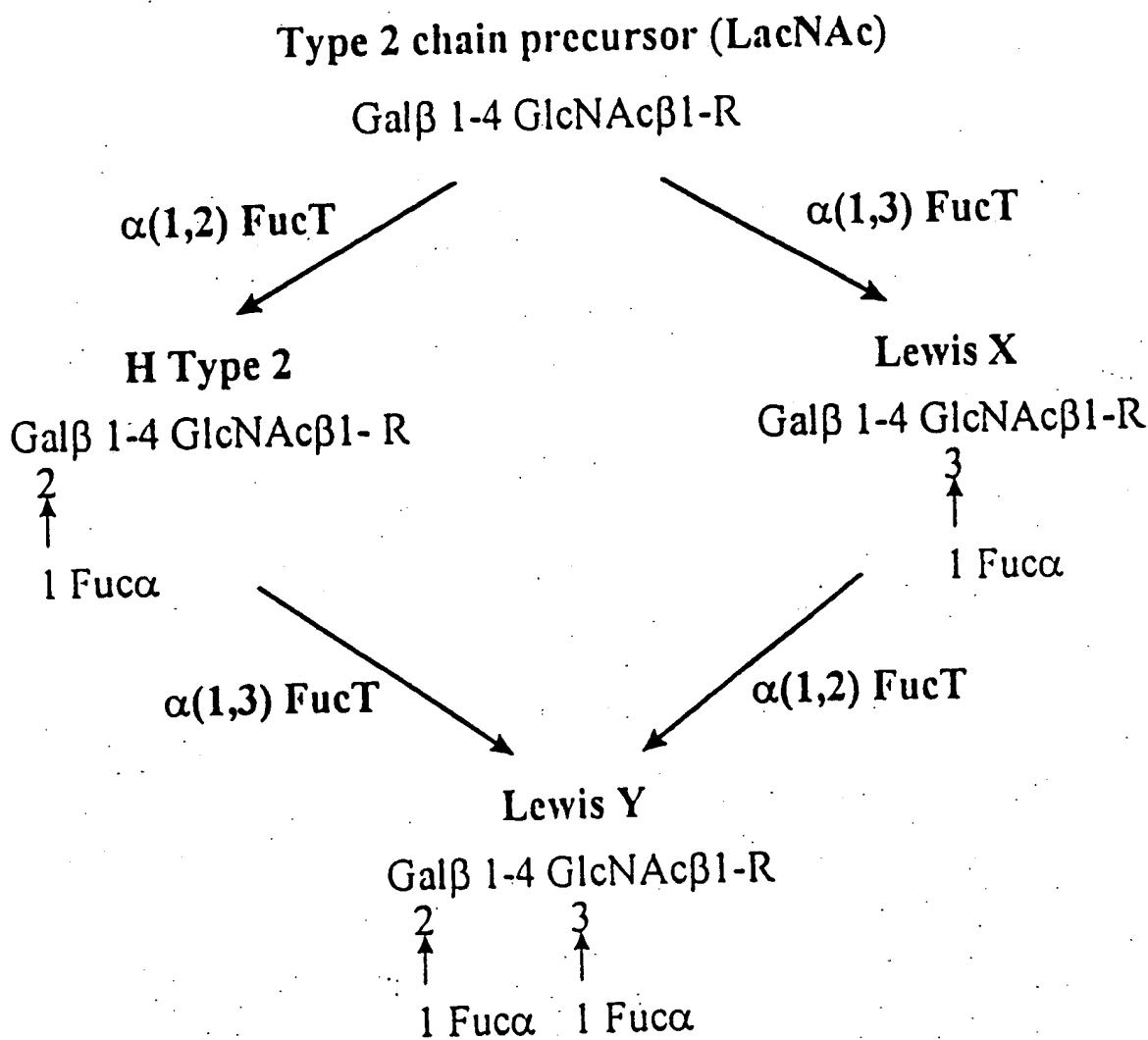


FIG. 5

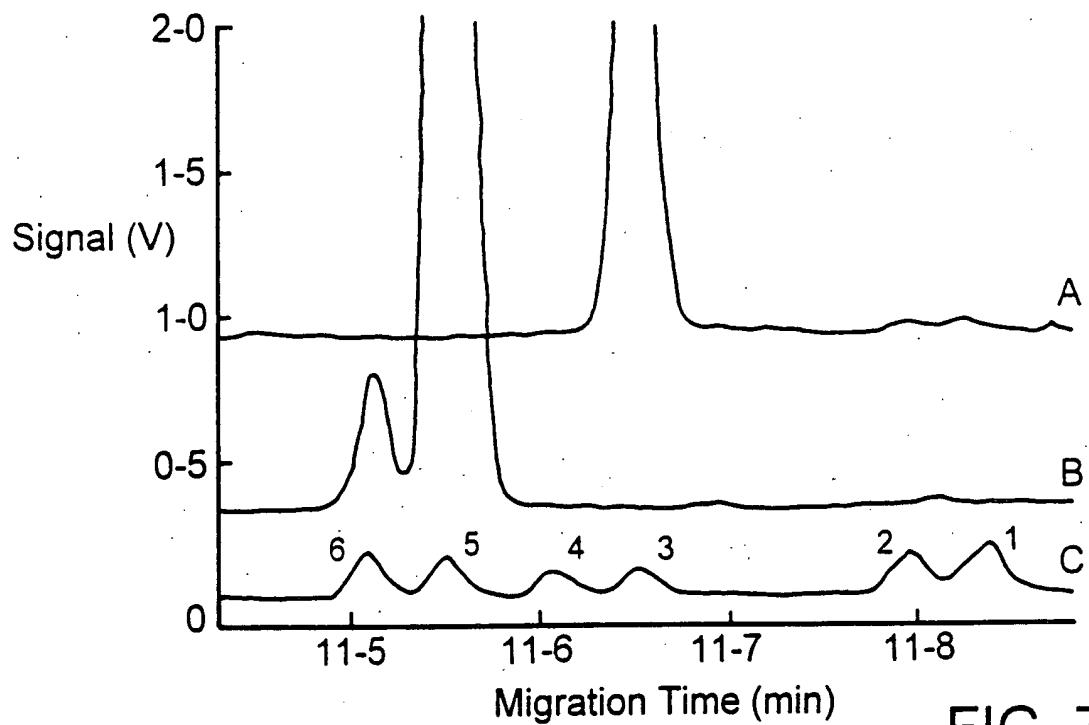


FIG. 7A

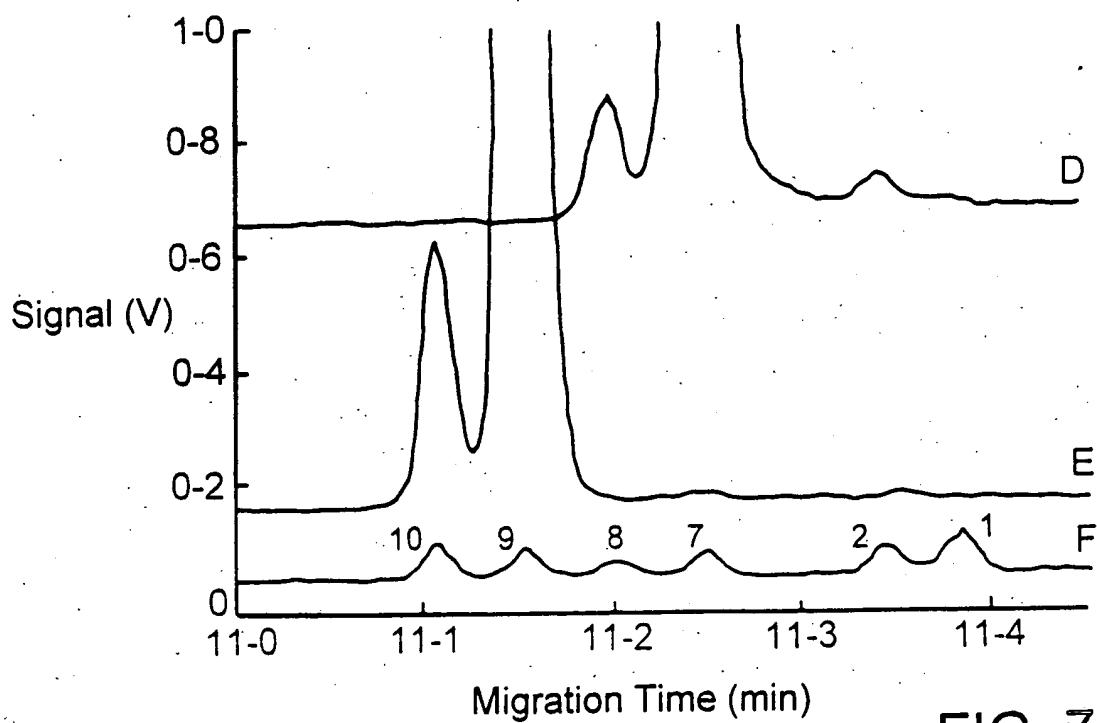


FIG. 7B

